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Date: February 1, 2006 **Time Sent:**

To:	Company:	Facsimile No:	Telephone No:
Examiner Marianne Allen	U.S. Patent and Trademark Office	571.273.0712	571.272.0712

From:	Cameron K. Weiffenbach	*Direct Phone:*	202.756.8171	
E-Mail:	cweiffenbach@mwe.com			
Sent By:	Jackie Reid-Johnson	*Direct Phone:*	202.756.8668	
Client/Matter/Tkpr:	050179-0081/05169	*Original to Follow by Mail:*		No
		Number of Pages, Including Cover:		32

Message:

U.S. Patent Application No.09/555,275
Art Unit 1631
Applicant: Bentley et al.

Dear Examiner Allen:

Attached is a copy of a document filed in the USPTO on February 5, 2002 along with evidence of receipt of the document by the USPTO. The document is a substitute sequence listing and a preliminary amendment. This document should take care of the printer query. Should you have any questions, please do not hesitate to call me.

Sincerely yours,
McDERMOTT WILL & EMERY, LLP

Cameron K. Weiffenbach
Registration No. 44,488

Diane Davis

Country Application

05-Feb-02

Client-Matter:	050179-0081	**Country:** US	**SubCase:**
Family Number:	050179-0081	United States of America	
Case Type:	PCT	**Application Status:**	Pending
Application Number:	09/555,275	**Filing Date:**	26-May-2000
Patent Number:		**Issue Date:**	
Publication Number:		**Publication Date:**	
Priority Number:	PP0585	**Priority Date:**	27-Nov-1997
Tax Schedule:	LE	**Expiration Date:**	
Reel & Frame:	010994/0301	**Tax Start Date:**	
Group Art Unit:		**ClientRef:**	92546
Agent:			
Agent Reference Number:			

List Of User Actions

Action(s) Due	Due Date	Action Taken
Office Action Received Yet?	26-Feb-2002 Due Date	
FILING RECEIPT RECD YET?	07-Mar-2002 Due Date	

Applicant: John David BENTLEY, et al. Docket No. 50179-081

Title/Mark: METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR Serial/Reg./Patent No. 09/555,275

Date Sent: 2/5/02 ☒ Hand Carried ☐ Fax ☐ Electronic ☐ Cert. of Mailing ☐ Express Mail No. _____

☐ Transmittal Letter

New Patent App ☒ Utility ☐ Design ☐ Cont. ☐ CIP ☐ Div. ☐ PCT ☐ CPA ☐ RCE ☐ Prov

☐ Other: _____

_____ pages of Specification

_____ pages of Claims

_____ pages of Abstract

_____ pages of Formal/Informal Drawings

☐ Small Entity ☐ Large Entity

☐ Declaration/Power of Attorney

☐ Recordation of Assignment/Security Agreement

☐ Information Disclosure Statement

_____ Form PTO 1449

_____ copies of cited references

☒ Preliminary Amendment

☐ Response to Missing Parts Notice

☐ Resp. to Notice to Correct App. Papers

OIPE JC174 FEB 0 5 2002 PATENT & TRADEMARK OFFICE

☐ Letter submitting _____ pages of drawings

☐ Req. for Approval of Drawing Amendments

☐ Req. for Oral Hearing

☐ Not. of Appeal ☐ Appeal Brief ☐ Reply Brief

☐ Rule 312 Amendment/Letter

☐ Req. for Acknowledgement of Cited Art

☐ Issue Fee

☐ Publication Fee

☐ Req. for Certificate of Correction

☐ Maintenance Fee for _____ years after grant

☐ Fee Address Indication Form _____

☐ Terminal Disclaimer

☐ Petition to Commissioner

☐ Status Inquiry

Other Submission of Substitute Sequence Listing, Preliminary Amendment, Diskette Containing Computer Readable

☒ Copy of Sequence Listing

☐ Certified Copy of Priority Doc.

☐ Claim for Convention Priority

☐ Response/Amendment to Office Action of _____ _____

☐ Request for _____-day/month Extension of Time

					KNW	Tkr #	6546	Secy. or PL:	DM, Davis

ANTI-STATIC
MEDIA MAILER

Applicant: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

Title: METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR

Attorney Docket: 050179-0081
Data Recorded: February 5, 2002

U.S. Serial NO.: 09/555,275
U.S. Filing Date: 26 May 2000

MS-DOS, ASCII Format

CAUTION
Do not bend or fold
Avoid exposure to all magnetic fields

Attorney Docket No. 050179-0081 **PATENT APPLICATION**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of	
John David BENTLEY, et al.	
Serial No.: 09/555,275	Group Art Unit: TBA
Filed: May 26, 2000	Examiner: TBA
For: METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR	

SUBMISSION OF SUBTITUTE SEQUENCE LISTING AND PRELIMINARY AMENDMENT

Honorable Assistant Commissioner for Patents
BOX SEQUENCE
Washington, D.C. 20231

Sir:

Prior to initial examination of the above-captioned patent application, please amend the above-captioned patent application as follows:

IN THE SPECIFICATION:

Please substitute the second paragraph on page 20 and continuing on to page 21 of the specification with the following rewritten paragraph.

-- Soluble IGF-1R/462 protein was recovered from harvested fermentation medium by affinity chromatography on columns prepared by coupling Mab 9E10 to divinyl sulphone-activated agarose beads (Mini Leak: Kem En Tec. Denmark) as recommended by the manufacturer. Mini-Leak Low and Medium affinity columns wieth antibody loadings of 1.5-4.5

mg/ml of hydrated matrix were obtained, with the loading range of 2.5-3 mg/ml giving optimal performance (data not shown). Mab 9E10 was produced by growing hybridoma cells (American Tissue Culture Collection) in serum-free medium in the Celligen Plus bioreactor and recovering the secreted antibody (4 g) using protein A glass beads (Prosep-A, bioprocessing Limited, USA). Harvested culture medium containing IGF-1R/462 protein was adjusted to pH 8.0 with Tris-HCl (Sigma), made 0.02% (w/v) in sodium azide and passed at 3-5 ml/min over 50 ml Mab 9E10 antibody columns at 4° C. Bound protein was recovered by recycling a solution of 2-10 mg of the undecamer c-myc peptide EQKLISEEDLN (SEQ ID NO. 16) (Hoogenboom et al., 1991) in 20 ml of Tris-buffered saline containing 0.02% sodium azide (TBSA). Between 65% and 75% of the product was recovered from the medium as estimated by ELISA, with a further 15-25% being recovered by a second pass over the columns. Peptide recirculation (~10 times) through the column eluted bound protein more efficiently than a single, slower elution. Residual bound protein was eluted with sodium citrate buffer at pH 3.0 into 1 M Tris HCl pH 8.0 to neutralize the eluant, and columns were re-equilibrated with TBSA.--

Please insert after page 46 and before the claims the attached paper copy of the this Substitute Sequence Listing.

REMARKS

The specification is corrected and a Substitute Sequence Listing is herein submitted to

comply with the requirements for an application containing a nucleotide and/or amino acid sequence.

Hereto is an attached Substitute Sequence Listing in paper and computer readable format. The paper copy and computer readable copy of the Substitute Sequence Listing are the same. The substitute Sequence Listing does not include new matter.

CONCLUSION

Entry of the Substitute Sequence Listing and favorable consideration are respectfully requested.

To the extent necessary, please grant any extension of time deemed necessary for entry of this communication. Please charge any deficient fees, or credit any overpayment of fees, to Deposit Account 500417.

Respectfully submitted,

McDermott, Will & Emery

Kelli N. Watson
Registration No. 47,170

DATE: February 5, 2002

Attorney Docket No. 050179-0081
Application Serial No. 09/555,275

McDermott, Will & Emery
600 Thirteenth Street, N.W.
Washington, D.C. 20005-3096
(202) 756-8351 (Telephone, direct)
(202) 756-8087 (Facsimile)

Attachments:

Paper Copy of Sequence Listing
Diskette Containing Computer Readable
Copy of Sequence Listing

Attorney Docket No. 050179-0081
Application Serial No. 09/555,275

ATTACHMENT

Version With Markings To Show Changes Made

IN THE SPECIFICATION

The second paragraph on page 20 and continuing on to page 21 of the specification is substituted with the following rewritten paragraph.

– Soluble IGF-1R/462 protein was recovered from harvested fermentation medium by affinity chromatography on columns prepared by coupling Mab 9E10 to divinyl sulphone-activated agarose beads (Mini Leak: Kem En Tec. Denmark) as recommended by the manufacturer. Mini-Leak Low and Medium affinity columns wieth antibody loadings of 1.5-4.5 mg/ml of hydrated matrix were obtained, with the loading range of 2.5-3 mg/ml giving optimal performance (data not shown). Mab 9E10 was produced by growing hybridoma cells (American Tissue Culture Collection) in serum-free medium in the Celligen Plus bioreactor and recovering the secreted antibody (4 g) using protein A glass beads (Prosep-A, bioprocessing Limited, USA). Harvested culture medium containing IGF-1R/462 protein was adjusted to pH 8.0 with Tris-HCl (Sigma), made 0.02% (w/v) in sodium azide and passed at 3-5 ml/min over 50 ml Mab 9E10 antibody columns at 4° C. Bound protein was recovered by recycling a solution of 2-10 mg of the undecamer c-myc peptide EQKLISEEDLN (SEQ ID NO. 16) (Hoogenboom et al., 1991) in 20 ml of Tris-buffered saline containing 0.02% sodium azide (TBSA). Between 65% and 75% of the product was recovered from the medium as estimated by ELISA, with a further 15-25% being

recovered by a second pass over the columns. Peptide recirculation (~10 times) through the column eluted bound protein more efficiently than a single, slower elution. Residual bound protein was eluted with sodium citrate buffer at pH 3.0 into 1 M Tris HCl pH 8.0 to neutralize the eluant, and columns were re-equilibrated with TBSA.--

The attached paper copy of this Substitute Sequence Listing is inserted after page 46 and before the claims of the specification.

SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organisation

<120> Method of Designing Agonists and Antagonists to IGF Receptor

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<140> 09/555,275
<141> 2000-05-26

<150> PCT/AU98/00998
<151> 1998-11-27

<150> PP2598
<151> 1998-03-25

<150> PP0585
<151> 1997-11-27

<160> 16

<170> PatentIn version 3.1

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        35                  40                  45

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65                  70                  75                  80

Leu Phe Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys
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Leu Ser Phe Pro Lys Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe
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Arg Val Tyr Gly Leu Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr
65 70 75 80

Val Ile Arg Gly Ser Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe
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Glu Met Val His Leu Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile
100 105 110

Thr Arg Gly Ser Val Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu
115 120 125

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Val Leu Ile Ala Leu Asn Thr Val Glu Arg Ile Pro Leu Glu Asn Leu
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Gln Ile Ile Arg Gly Asn Met Tyr Tyr Glu Asn Ser Tyr Ala Leu Ala
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Val Leu Ser Asn Tyr Asp Ala Asn Lys Thr Gly Leu Xaa Xaa Lys Pro
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115 120 125

Asn Pro Ala Leu Cys Asn Val Glu Ser Ile Gln Trp Arg Asp Ile Val
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Gly Ser Cys Gln Lys
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Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val
50 55 60

Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg
65 70 75 80

Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr
85 90 95

Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr
100 105 110

Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile
115 120 125

Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys
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50 55 60

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65 70 75 80

Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn
85 90 95

Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Ile
100 105 110

Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser
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20 25 30

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35 40 45

Met Gly Leu Ile Glu Val Val Thr Gly Tyr Val Lys Ile Arg His Ser
50 55 60

His Ala Leu Val Ser Leu Ser Phe Leu Lys Asn Leu Arg Leu Ile Leu
65 70 75 80

Gly Glu Glu Gln Leu Glu Gly Asn Tyr Ser Phe Tyr Val Leu Asp Asn
85 90 95

Gln Asn Leu Gln Gln Leu Trp Asp Trp Asp His Arg Asn Leu Thr Ile
100 105 110

Lys Ala Gly Lys Met Tyr Phe Ala Phe Asn Pro Lys Leu Cys Val Ser
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Ser

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35 40 45

Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser Ala Pro Asp
50 55 60

Asn Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Tyr Ala Gly Val
65 70 75 80

Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu Gly Trp Arg
85 90 95

Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala Glu Ser Ser
100 105 110

Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met Gln Glu Cys
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        35                  40                  45

Gly Leu Cys Cys His Ser Glu Cys Leu Gly Asn Cys Ser Gln Pro Asp
    50                  55                  60

Asp Pro Thr Lys Cys Val Ala Cys Arg Asn Phe Tyr Leu Asp Gly Arg
65                  70                  75                  80

Cys Val Glu Thr Cys Pro Pro Pro Tyr Tyr His Phe Gln Asp Trp Arg
                85                  90                  95

Cys Val Asn Phe Ser Phe Cys Gln Asp Leu His His Lys Cys Lys Asn
            100                 105                 110

Ser Arg Arg Gln Gly Cys His Gln Tyr Val Ile His Asn Asn Lys Cys
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Gly Arg Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys
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35 40 45

Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg
50 55 60

Lys Phe Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met
65 70 75 80

Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys
85 90 95

Tyr Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val
100 105 110

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Cys Arg
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35 40 45

Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met
50 55 60

Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala
65 70 75 80

His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val
85 90 95

Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His
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Leu Ile Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu
35 40 45

Thr Val Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu
50 55 60

Ser Leu Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys
65 70 75 80

Leu Phe Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys
85 90 95

Asp Ile Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg
100 105 110

Ile Glu Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser
115 120 125

Leu Ile Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro

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            420                 425                 430

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660 665 670

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770 775 780

Cys Ser Ala Ser Asn Phe Val Phe Ala Arg Thr Met Pro Ala Glu Gly
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805 810 815

Ser Ile Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile
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Leu Thr Arg Leu His Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His
20 25 30

Leu Gln Ile Leu Leu Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp
35 40 45

Leu Ser Phe Pro Lys Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe
50 55 60

Arg Val Tyr Gly Leu Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr
65 70 75 80

Val Ile Arg Gly Ser Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe
85 90 95

Glu Met Val His Leu Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile
100 105 110

Thr Arg Gly Ser Val Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu
115 120 125

Ala Thr Ile Asp Trp Ser Arg Ile Leu Asp Ser Val Glu Asp Asn Tyr
130 135 140

Ile Val Leu Asn Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly
145 150 155 160

Thr Ala Lys Gly Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln
165 170 175

Phe Val Glu Arg Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro
180 185 190

Thr Ile Cys Lys Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His
195 200 205

Ser Glu Cys Leu Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys
210 215 220

Val Ala Cys Arg Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys
225 230 235 240

Pro Pro Pro Tyr Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser
245 250 255

Phe Cys Gln Asp Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly
260 265 270

Cys His Gln Tyr Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro
275 280 285

Ser Gly Tyr Thr Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu
290 295 300

Gly Pro Cys Pro Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile
305 310 315 320

Asp Ser Val Thr Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn
325 330 335

Gly Ser Leu Ile Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu
340 345 350

Leu Glu Ala Asn Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys
355 360 365

Ile Arg Arg Ser Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu
370 375 380

Arg Leu Ile Arg Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr
385 390 395 400

Ala Leu Asp Asn Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His
405 410 415

Asn Leu Thr Ile Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys
420 425 430

Leu Cys Leu Ser Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys
435 440 445

Gly Arg Gln Glu Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Gln
450 455 460

Ala Ser Cys Glu Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser
465 470 475 480

Phe Asp Lys Ile Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe
485 490 495

Arg Asp Leu Leu Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln
500 505 510

Asn Val Thr Glu Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp
515 520 525

Thr Val Val Asp Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser
530 535 540

Gln Asn His Pro Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln
545 550 555 560

Tyr Ala Ile Phe Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg
565 570 575

Thr Tyr Gly Ala Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr
580 585 590

Asn Pro Ser Val Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser
595 600 605

Gln Ile Ile Leu Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile
610 615 620

Thr His Tyr Leu Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu
625 630 635 640

Phe Glu Leu Asp Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr
645 650 655

Trp Ser Pro Pro Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser
660 665 670

Glu Tyr Glu Asp Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp
675 680 685

Ser Gln Ile Leu Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe
690 695 700

Glu Asp Tyr Leu His Asn Val Val Phe Val Pro Arg Pro Ser Arg Lys
705 710 715 720

Arg Arg Ser Leu Gly Asp Val Gly Asn Val Thr Val Ala Val Pro Thr
725 730 735

Val Ala Ala Phe Pro Asn Thr Ser Ser Thr Ser Val Pro Thr Ser Pro
740 745 750

Glu Glu His Arg Pro Phe Glu Lys Val Val Asn Lys Glu Ser Leu Val
755 760 765

Ile Ser Gly Leu Arg His Phe Thr Gly Tyr Arg Ile Glu Leu Gln Ala
770 775 780

Cys Asn Gln Asp Thr Pro Glu Glu Arg Cys Ser Val Ala Ala Tyr Val

785 790 795 800

Ser Ala Arg Thr Met Pro Glu Ala Lys Ala Asp Asp Ile Val Gly Pro
805 810 815

Val Thr His Glu Ile Phe Glu Asn Asn Val Val His Leu Met Trp Gln
820 825 830

Glu Pro Lys Glu Pro Asn Gly Leu Ile Val Leu Tyr Glu Val Ser Tyr
835 840 845

Arg Arg Tyr Gly Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His
850 855 860

Phe Ala Leu Glu Arg Gly Cys Arg Leu Arg Gly Leu Ser Pro Gly Asn
865 870 875 880

Tyr Ser Val Arg Ile Arg Ala Thr Ser Leu Ala Gly Asn Gly Ser Trp
885 890 895

Thr Glu Pro Thr Tyr Phe Tyr Val Thr Asp Tyr Leu Asp Val Pro Ser
900 905 910

Asn Ile Ala Lys
915

<210> 13
<211> 895
<212> PRT
<213> Homo sapiens

<400> 13

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Arg Gln Leu Glu Asn Cys Ser Val Val Glu Gly His Leu Gln Ile Leu
20 25 30

Leu Met Phe Thr Ala Thr Gly Glu Asp Phe Arg Gly Leu Ser Phe Pro
35 40 45

Arg Leu Thr Gln Val Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly
50 55 60

Leu Glu Ser Leu Arg Asp Leu Phe Pro Asn Leu Ala Val Ile Arg Gly
65 70 75 80

Thr Arg Leu Phe Leu Gly Tyr Ala Leu Val Ile Phe Glu Met Pro His
85 90 95

Leu Arg Asp Val Ala Leu Pro Ala Leu Gly Ala Val Leu Arg Gly Ala
100 105 110

Val Arg Val Glu Lys Asn Gln Glu Leu Cys His Leu Ser Thr Ile Asp
115 120 125

Trp Gly Leu Leu Gln Pro Ala Pro Gly Ala Asn His Ile Val Gly Asn
130 135 140

Lys Leu Gly Glu Glu Cys Ala Asp Val Cys Pro Gly Val Leu Gly Ala
145 150 155 160

Ala Gly Glu Pro Cys Ala Lys Thr Thr Phe Ser Gly His Thr Asp Tyr
165 170 175

Arg Cys Trp Thr Ser Ser His Cys Gln Arg Val Cys Pro Cys Pro His
180 185 190

Gly Met Ala Cys Thr Ala Arg Gly Glu Cys Cys His Thr Glu Cys Leu
195 200 205

Gly Gly Cys Ser Gln Pro Glu Asp Pro Arg Ala Cys Val Ala Cys Arg
210 215 220

His Leu Tyr Phe Gln Gly Ala Cys Leu Trp Ala Cys Pro Pro Gly Thr
225 230 235 240

Tyr Gln Tyr Glu Ser Trp Arg Cys Val Thr Ala Glu Arg Cys Ala Ser
245 250 255

Leu His Ser Val Pro Gly Arg Ala Ser Thr Phe Gly Ile His Gln Gly
260 265 270

Ser Cys Leu Ala Gln Cys Pro Ser Gly Phe Thr Arg Asn Ser Ser Ser
275 280 285

Ile Phe Cys His Lys Cys Glu Gly Leu Cys Pro Lys Glu Cys Lys Val
290 295 300

Gly Thr Lys Thr Ile Asp Ser Ile Gln Ala Ala Gln Asp Leu Val Gly
305 310 315 320

Cys Thr His Val Glu Gly Ser Leu Ile Leu Asn Leu Arg Gln Gly Tyr
325 330 335

Asn Leu Glu Pro Gln Leu Gln His Ser Leu Gly Leu Val Glu Thr Ile
340 345 350

Thr Gly Phe Leu Lys Ile Lys His Ser Phe Ala Leu Val Ser Leu Gly
355 360 365

Phe Phe Lys Asn Leu Lys Leu Ile Arg Gly Asp Ala Met Val Asp Gly
370 375 380

Asn Tyr Thr Leu Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Gly
385 390 395 400

Ser Trp Val Ala Ala Gly Leu Thr Ile Pro Val Gly Lys Ile Tyr Phe
405 410 415

Ala Phe Asn Pro Arg Leu Cys Leu Glu His Ile Tyr Arg Leu Glu Glu
420 425 430

Val Thr Gly Thr Arg Gly Arg Gln Asn Lys Ala Glu Ile Asn Pro Arg
435 440 445

Thr Asn Gly Asp Arg Ala Ala Cys Gln Thr Arg Thr Leu Arg Phe Val
450 455 460

Ser Asn Val Thr Glu Ala Asp Arg Ile Leu Leu Arg Trp Glu Arg Tyr
465 470 475 480

Glu Pro Leu Glu Ala Arg Asp Leu Leu Ser Phe Ile Val Tyr Tyr Lys
485 490 495

Glu Ser Pro Phe Gln Asn Ala Thr Glu His Val Gly Pro Asp Ala Cys
500 505 510

Gly Thr Gln Ser Trp Asn Leu Leu Asp Val Glu Leu Pro Leu Ser Arg

515 520 525

Thr Gln Glu Pro Gly Val Thr Leu Ala Ser Leu Lys Pro Trp Thr Gln
530 535 540

Tyr Ala Val Phe Val Arg Ala Ile Thr Leu Thr Thr Glu Glu Asp Ser
545 550 555 560

Pro His Gln Gly Ala Gln Ser Pro Ile Val Tyr Leu Arg Thr Leu Pro
565 570 575

Ala Ala Pro Thr Val Pro Gln Asp Val Ile Ser Thr Ser Asn Ser Ser
580 585 590

Ser His Leu Leu Val Arg Trp Lys Pro Pro Thr Gln Arg Asn Gly Asn
595 600 605

Leu Thr Tyr Tyr Leu Val Leu Trp Gln Arg Leu Ala Glu Asp Gly Asp
610 615 620

Leu Tyr Leu Asn Asp Tyr Cys His Arg Gly Leu Arg Leu Pro Thr Ser
625 630 635 640

Asn Asn Asp Pro Arg Phe Asp Gly Glu Asp Gly Asp Pro Glu Ala Glu
645 650 655

Met Glu Ser Asp Cys Cys Pro Cys Gln His Pro Pro Pro Gly Gln Val
660 665 670

Leu Pro Pro Leu Glu Ala Gln Glu Ala Ser Phe Gln Lys Lys Phe Glu
675 680 685

Asn Phe Leu His Asn Ala Ile Thr Ile Pro Ile Ser Pro Trp Lys Val
690 695 700

Thr Ser Ile Asn Lys Ser Pro Gln Arg Asp Ser Gly Arg His Arg Arg
705 710 715 720

Ala Ala Gly Pro Leu Arg Leu Gly Gly Asn Ser Ser Asp Phe Glu Ile
725 730 735

Gln Glu Asp Lys Val Pro Arg Glu Arg Ala Val Leu Ser Gly Leu Arg
740 745 750

His Phe Thr Glu Tyr Arg Ile Asp Ile His Ala Cys Asn His Ala Ala
755 760 765

His Thr Val Gly Cys Ser Ala Ala Thr Phe Val Phe Ala Arg Thr Met
770 775 780

Pro His Arg Glu Ala Asp Gly Ile Pro Gly Lys Val Ala Trp Glu Ala
785 790 795 800

Ser Ser Lys Asn Ser Val Leu Leu Arg Trp Leu Glu Pro Pro Asp Pro
805 810 815

Asn Gly Leu Ile Leu Lys Tyr Glu Ile Lys Tyr Arg Arg Leu Gly Glu
820 825 830

Glu Ala Thr Val Leu Cys Val Ser Arg Leu Arg Tyr Ala Lys Phe Gly
835 840 845

Gly Val His Leu Ala Leu Leu Pro Pro Gly Asn Tyr Ser Ala Arg Val
850 855 860

Arg Ala Thr Ser Leu Ala Gly Asn Gly Ser Trp Thr Asp Ser Val Ala
865 870 875 880

Phe Tyr Ile Leu Gly Pro Glu Glu Glu Asp Ala Gly Gly Leu His
885 890 895

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<212> DNA
<213> Artificial sequence

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tcgacgtc 68

<210> 15
<211> 18
<212> PRT
<213> Homo sapiens

<400> 15

Asp Val Asp Asp Asp Asp Lys Glu Gln Lys Leu Ile Ser Glu Glu Asp
1 5 10 15

Leu Asn

<210> 16
<211> 11
<212> PRT
<213> Homo sapiens

<400> 16

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10